

U.S.-08-429-998-4

Sequence 4, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plovman, Gregory D.
TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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Alignment Scores:		
Pred. No.:	6,92e-217	Length:
Score:	3472.00	Matches:
Percent Similarity:	98.99%	Conservative:
Best Local Similarity:	98.99%	Mismatches:
Query Match:	84.62%	Indels:
DB:	2	Gaps:

US-09-880-842-16 (1-2095) x US-08-429-998-4 (1-593)

Qy	13	ATGTGGACCCGTGGTGGCTGGCTTAAACACAGCGGCTGTGTGCTGGAAAGCGGGTGC	72
Db	1	MetTrpThrLeuValSerTrpValAlaLeuThrAlaGlyLeuValAlaGlyThrArgCys	20
Qy	73	CCAGATGTCAGTCTGTGCCCTGTGCCCTGTGCACCCCGAGAGCAGCAGCTACAGC	132
Db	21	ProAspGlyInpHecysProValAlaCysCysLeuAspProGlyAlaSerTyrSer	40
Qy	133	TGCTGCCGTCCCTTCTGGCAAAATGGCCCCAACACTGACGAGGCATCTGGTGGCCCC	192
Db	41	CysCysArgProLeuLeuAspIstPProThrThrLeuSerArgHisLeuGlyGlyPro	60
Qy	193	TGCCAGTTGTAGCCCATCTGTCTGCCGGCCACCTCTGCATCTTTACCTGCTCAGGACT	252
Db	61	CysGlnValAspAlaHisCysSerAlaGlyHisSerCysIlePheThrValSerGlyThr	80
Qy	253	TCAAGTTGTGCCCTTCCCAAGCCCGTGCATGCGGGATGGCCATCACTGCTGCCCA	312
Db	81	SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHisIstCysCysPro	100

Db	321	CysCysProAlaGlyPheThrCysAspThrGlnLysGlyThrCysGluGlnGlyProHis	340
Qy	1033	CAGTGCCTCGGATGGAGAAAGCCCAAGCTCACCTCAGCCTGCAGACCCACACAGCCCTTG	1092
Db	341	GlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeu	360
Qy	1093	AAGAGAGATGTCCTCTGTGATATGTTCAGAGAGCTGTCCCTCTCCGATACCTGCTGCCAA	1152
Db	361	LysArgAspValProCysAspAsnValSerSerCysProSerSerAspThrCysCysGln	380
Qy	1153	CTCAGCTCTGGGAGTGGGGCTGTCTGCATCCAGAGAGCTGTCTGCTGCTCGGACCA	1212
Db	381	LeuThrSerGlyGluTrpGlyCysCysProIleProGluAlaValCysCysSerAspHis	400
Qy	1213	CAGACATGCTGCCCCCAGCGATACATGTTGTAGCTGAGGGGCGAGTGTACGAGGAGGC	1272
Db	401	GlnHisCysCysProGlnGlyTyThrCysValAlaGluGlyGlnCysGlnArgGlySer	420
Qy	1273	GAGATCGTGTGTCACATGGAGAGATGCTGCCCGCGCGTTCCTTATCCCAACCCGAGA	1332
Db	421	GluIleValAlaGlyLeuGluLysMetProAlaArgAlaSerLeuSerHisProArg	440
Qy	1333	GACATCGGCTGTGACCAGCACACAGATGCCCCGGTGGCGGAACTGCTGCCCGAGCCAG	1392
Db	441	AspIleGlyCysAspGlnHisThrSerCysProValGlyGlnThrCysCysProSerLeu	460
Qy	1393	GGTGGAGCTGGGCTGCTGCCAGTTCGCCCATGCTGCTGTGCTGCGAGGATCCCGAC	1452
Db	461	GlyGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis	480
Qy	1453	TGTTGCCCGGTGGCTACACGTCAACGTGAAGGCTCGATCTCTCGAGAAAGAGTGCTC	1512
Db	481	CysCysProAlaGlyTyThrCysAsnValLysAlaArgSerCysGluLysGluValVal	500
Qy	1513	TCTGCCACGCTGCCACCTTCTGGCCCGTAGCCCTCACGTGGGTGTGAAGAGCTGGAG	1572
Db	501	SerAlaGlnProAlaThrPheLeuAlaArgSerProHisValGlyValLysAspValGlu	520
Qy	1573	TGTGGGAAAGACACTTCTGCATGATAACACAGACCTGTCTCGCGAGACAAACCCAGGGC	1632
Db	521	CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysArgAspAsnArgGlnGly	540
Qy	1633	TGGGCTGTGTTCCCTTAGCCCGCAGGGCGTCTGTTGTCTGATCGGCGCCACTGCTGTCT	1692
Db	541	TrpAlaCysCysProTyTrpArgGlnGlyValCysCysAlaAspArgHisCysCysPro	560
Qy	1693	GCTGGCTTCGCTCGCACCGCAGGGGTACCAAGTGTGTCGCGAGGAGGCCCGCGCTGG	1752
Db	561	AlaGlyPheArgCysAlaAlaArgGlyThrLysCysLeuArgArgGluAlaProArgTrp	580
Qy	1753	GACGCCCTTTGAGGAGCCCGCTTCGAGACAGCTGCTG	1791
Db	581	AspAlaProLeuArgAspProAlaLeuArgGlnLeuLeu	593

RESULT 6

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PCT-US91-02321-4
; Sequence 4, Application PC/TUS9102321
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plowman, Gregory D.
; TITLE OF INVENTION: EPIITELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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US-08-429-998-2

Alignment Scores:

9.94e-167	Length:	589
2696.00	Matches:	443
84.15%	Conservative:	56
74.70%	Mismatches:	90
75.71%	Indels:	4
2	Gaps:	3
DB:		

US-09-880-842-16 (1-2095) x US-08-429-998-2 (1-589)

QY	13	ATGTGACCCCTGGTGAAGCTGGGTGGCGCTTTAACAGACAGGGCTGTGTCTGGAAACGGCGTGC	72
Db	1	MetTrrIleLeuValSerTrpLeuAlaLeuValAlaArgLeuValAlaGlyThrGlnCys	20
QY	73	CCAGATGGTCAGTTCTGCGCTGGCGCTGTGCTGAGACCCCGAGAGCAGCTACAGC	132
Db	21	ProAspGlyGlnPheCysProValAlaCysCysLeuAspGlnGlyAlaSerTyrSer	40
QY	133	TGCTGCCGTCCTCTTCTGGACAAATGGGCCAACACTGAGCAGGCATCTGGGTGGCCCC	192
Db	41	CysCysAsnProLeuLeuAspThrTrpProIleIleThrSerArgArgLeuAspGlySer	60
QY	193	TGCCAGGTGTAGCCCACTGCTCTCCGGCCACATCCCTGCATCTTACCGTTCAGGACT	252
Db	61	CysGlnIleArgAspHisCysProAspGlyTyrSerCysLeuLeuThrValSerGlyThr	80
QY	253	TCAGTTGTGTCCTCTCCACAGACCCGTGCATGCGGGGATGGCCACTCACTGCTGCCCA	312
Db	81	SerSerCysCysProPheSerGluGlyValSerCysAspGlyGlnHisCysCysPro	100
QY	313	CGGGGCTTCACCTGAGTGCAGAGCGGCGATCCCTTCCAAAGATCAGGTAACTACCTC	372
Db	101	ArgGlyPheHisCysSerAlaAspGlyIysSerCysSerGlnIleSer--AspSerLeu	119
QY	373	GTGGGTGCCATCCAGTGGCCCTCATAGTCAGTTCCGAATGCCCGGACTTCTCCACGTCTGT	432
Db	120	LeuGlyAlaValGlnCysProGlySerGlnPheGluCysProAspSerAlaThrCysCys	139
QY	433	GTTATGGTCGATGGCTCTGGGGGTGTCGCCCATGCCAGGCTTCCTGCTGTGAGAC	492
Db	140	IleMetIleAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp	159
QY	493	AGGGTCACCTGTGTCGGCAGCGTGCTTCGCCACCTGTTCACACCCGGCTGCATCAC	552
Db	160	ArgValHisCysCysProHisGlyAlaSerCysAspLeuValHisThrArgCysIleSer	179
QY	553	CCACCGGGCACCAACCCCTGGCAAGAAGTCCCTGCCCAGAGGACTAACAGGGCAGTG	612
Db	180	ProThrGlyThrHisProLeuLeuIlysPheProAlaGlnArgThrAsnArgAlaVal	199
QY	613	GCCTTGTCCAGCTCGGTCTATGTCCGACACACAGTCCCGGTGCCCTGATGTTCTAAC	672
Db	200	AlaPheProPheSerValValCysProAspAlaIlysThrGlnCysProAspAspSerThr	219
QY	673	TGCTGTGAGCTGCCAGTGGGAAGTATGGCTGCTGCCAAATGCCCAACGCCACTGCTGC	732
Db	220	CysCysGluLeuProThrGlyIysTyrGlyCysCysProMetProAsnAlaIleCysCys	239
QY	733	TCCGATCACCTGCACGTGCCCCCAAGACACTGTGTGACCTGATCAGCAGCTAAGTGC	792
Db	240	SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerIlysCys	259
QY	793	CTCTCCAAGAGAACCTACACGAGCACTCTCTCACTAAGCTGCCTGGCGCACAGTGGGC	852
Db	260	IleSerLysAsp--TyrThrThrAspLeuMetThrLysLeuProGlyTyrProValAsn	278
QY	853	GATGTGAATGTACATGAGGTGAGCTGCCAGATGGCTATACCTGCTCCGCTCTACAG	912
Db	279	GluValIysCysAspLeuValSerCysProAspGlyTyrThrCysCysArgLeuAsn	298
QY	913	TCGGGGGCTCGGGGCTGCGCTTTTACCACAGGCTGTGCTGTGAGGACCACTACAC	972

Db 517 CysGlyAlaGlyHisPheCysHisAspAsnGlnSerCysCysLeuAspSerGlnGlyGly 536
QY 1633 TGGCGCTGCTGCTCCCTACGCCAGGCGCTGTTGTGCTGATCGCGCGCCACTGCTGCTCT 1692
Db 537 TrpAlaCysCysProGlyValCysCysCysAspGlyArgHisCysCysPro 556
QY 1693 GCTGGCTTCGCTGCCACGACGAGGTACCAAGTGTTCGCGAGGAGGCCCGCGCTGG 1752
Db 557 IleGlyPheHisCysSerAlaGlyThrLysCysLeuArgLysLysThrProArgTrp 576
QY 1753 GAGCGCCCTTGGAGGACCGCGCTTGAGACAGCTGCTG 1791
Db 577 AspIleLeuLeuArgAspProAlaProA-gProLeuLeu 589

RESULT 10

PCT-US91-02321-2
; Sequence 2, Application PC/TUS9102321
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plowman, Gregory D.
; TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02321
; FILING DATE: 19910403
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0071A-PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)728-4800
; TELEFAX: (206)448-4775
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 589 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02321-2

Alignment Scores:
Pred. No.: 9,94e-167 Length: 589
Score: 2696.00 Matches: 443
Percent Similarity: 84.15% Conservative: 56
Best Local Similarity: 74.70% Mismatches: 90
Query Match: 65.71% Indels: 4
DB: 5 Gaps: 3

US-09-880-842-16 (1-2095) x PCT-US91-02321-2 (1-589)

QY 13 ATGTGGACCTGGTGGAGTGGGCTGTAAACAGAGGCTGGTGGTGGAGCGGTGC 72
Db 1 MetTrpIleLeuValSerTrpLeuAlaLeuValAlaArgLeuValAlaGlyThrGlnCys 20
QY 73 CCAGATGTGATGTCGCTGCTGGCTGCTGCTGGAGCCCGGAGGAGCCAGCTACAGC 132
Db 21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspGlnGlyAlaAsnTyrSer 40
QY 133 TGCTGCCCTCCCTCTTGGAACAATGGCCCAACACTGAGCAGGCATCTGGGTGGCCCC 192

Db 41 CysCysAsnProLeuLeuAspThrTrpProIleIleThrSerArgArgLeuAspGlySer 60
QY 193 TGCAGAGTTGATGCCACTGCTCTGCGCGGCACCTCTGCTGATCTTTACCGCTCAGGACT 252
Db 61 CysGlnIleArgAspHisCysProAspGlyTyrSerCysLeuLeuThrValSerGlyThr 80
QY 253 TCCAGTTGCTGCCCTTCCAGAGGCGCTGCGATGCGGGGATGGCCATCATCTGCTGCCCA 312
Db 81 SerSerCysCysProPheSerGluGlyValSerCysAspAspGlyGlnHisCysCysPro 100
QY 313 CGGGGCTTCCACTGCAGTGCAGAGCGCGGATCTCTTCCAAAGATCAGGTAAACAATCC 372
Db 101 ArgGlyPheHisCysSerAlaAspGlyLysSerCysSerGlnIleSer---AspSerLeu 119
QY 373 GTGGTGCCATCCAGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 432
Db 120 LeuGlyAlaValGlnCysProGlySerGlnPheGlyCysProAspSerAlaThrCysCys 139
QY 433 GTTATGTCGATGCTCTGCGGGTGTGCGCCATGCCAGGCTTCTGCTGTGAAGAC 492
Db 140 IleMetIleAspGlySerTrpGlyCysProMetProGlnAlaSerCysCysGluAsp 159
QY 493 AGGGTGCACTGCTCTCCGACGGTCTCTGCGACCTGCTGACCTGCTGACCTGCTGATCACA 552
Db 160 ArgValHisCysCysProHisGlyAlaSerCysAspLeuValHisThrArgCysIleSer 179
QY 553 CCCAGGCGCACCCCGCTGGCAAGAGCTCTCCCGCAGAGAGCTTACAGGCGCAGTG 612
Db 180 ProThrGlyThrHisProLeuLeuLysPheProAlaGlnArgThrAsnArgAlaVal 199
QY 613 GCCTGTGCCAGTCTGCTCCGACGAGTCCCGGTCGCGCTGCTGCTGCTGCTGCTGCTGCTG 672
Db 200 AlaPheProPheSerValValCysProAspAlaLysThrGlnCysProAspAspSerThr 219
QY 732 TCGTGTGAGTCCGAGTGGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Db 220 CysCysGluLeuProThrGlyLysTyrGlyCysCysProMetProAsnAlaIleCysCys 239
QY 733 TCCGATCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792
Db 240 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys 259
QY 793 CTCTCCAAAGGAGAGCGTACACGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 852
Db 260 IleSerLysAsp---TyrThrThrAspLeuMetThrLysLeuProGlyTyrProValAsn 278
QY 853 GATGTGAATGTGACATGAGTGGAGTGGCCAGATGGCTATACCTGCTGCTGCTGCTGCTGCT 912
Db 279 GluValLysCysAspLeuGluValSerCysProAspGlyTyrThrCysCysArgLeuAsn 298
QY 913 TCGGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
Db 299 ThrGlyAlaTrpGlyCysCysProPheThrLysAlaValCysCysGluAspHisIleHis 318
QY 973 TGCTGCTCCGCGGGGTTTACGTGTGACAGCAGAGGCTTCTGTAACAGGCGGCCCCAC 1032
Db 319 CysCysProAlaGlyPheGlnCysHisThrGlnThrGlyThrCysGluLeuGlyValLeu 338
QY 1033 CAGGTGCTGCTGATGGAGAGCGCCCGCTCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTG 1092
Db 339 GlnValProTrpMetLysLysValThrAlaSerLeuSerLeuProAspProGlnIleLeu 358
QY 1093 AAGAGAGATGCTCCCTGTGATAATGTGACAGCTGCTCCCTGCTGCTGCTGCTGCTGCTGCT 1152
Db 359 LysAsnAspValProCysAspAspPheSerCysProSerAsnAsnThrCysCysArg 378
QY 1153 CTCAGCTCTGGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1212
Db 379 LeuSerSerGlyAspTrpGlyCysCysProIleProGluAlaValCysCysLeuAspHis 398
QY 1213 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272

140	Db	11eMetValaspGlySerTrpGlyCysCysProMetProGlnAlaSerCysGluAsp	159
493	QY	AGSGTCACTGCTGTCGGACACGGTGCCTTCGGACCTGCTGTTACACACCGCTGCATCACCA	552
160	Db	ArgValHisCysCysProHisGlyAlaSerCysAspLeuValHisThrArgCysValSer	179
553	QY	CCACAGGGACCCACCCCTGGCAAGAAGCTCCCTGCCACGAGGACTAACAGGCGAGTG	612
180	Db	ProThrGlyThrHisThrLeuLeuLysLysPheProAlaGlnLysThrAsnArgAlaVal	199
613	QY	GCCTTGCCAGCTCGGTTCATGTGTCGGAGCACGGTCCCGGTGCCCTGATGGTCTACCC	672
200	Db	SerLeuProPheSerValValCysProAspAlaLysThrGlnCysProAspAspSerThr	219
673	QY	TGCTGTGAGTGCCTCCAGTGGGAAGTAGTGGTGTCTGCCCAATGCCAACGCCACCTGCTGC	732
220	Db	CysCysGluLeuProThrGlyLysTyrGlyCysCysProMetProAsnAlaIleCysCys	239
733	QY	TCCGATCACCTGCATGCTCCCCCAGACACATGTTGTGTGACCTGATCCAGTAGTAGTGC	792
240	Db	SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys	259
793	QY	CTCTCCAAAGAGAACGCTACACAGGACCTCTCACTAAGCTGCTCGCACACAGTGGGCG	852
260	Db	LeuSerLys--AsnTyrThrThrAspLeuLeuThrLysLeuProGlyTyrProValLys	278
853	QY	GATGTGAAATGTGACATGGAGGTGAGTGCACAGATGGCTATACCTGCTGCCCTCTACAG	912
279	Db	GluValLysCysAspMetGluValSerCysProGluGlyTyrThrCysCysArgLeuAsn	298
913	QY	TCGGGGCCTCGGGCTGCTCCCTTTTACCAGGCTGTGTGCTGAGACACCATACAC	972
299	Db	ThrGlyAlaTrpGlyCysCysProPheAlaLysAlaValCysCysGluAspHisIleHis	318
973	QY	TGCTGTCCCCGGGGTTTACGTGTGACACGACGAAGGGTACCTGTGAACAGGGGCCCCAC	1032
319	Db	CysCysProAlaGlyPheGlnCysHisThrGluLysGlyThrCysGluMetGlyIleLeu	338
1033	QY	CAGTGCCTCGGATGGAGAGAGGCCACCACTCAGCTGCCACACCCACCAAGCCTTG	1092
339	Db	GlnValProTrpMetLysLysValIleAlaProArgLeuProAspProGlnIleLeu	358
1093	QY	AAGAGAGATGTCCCTCTGATAATGTACAGAGCTGTCCCTCCCTCCGATACCTCTGCCAC	1152
359	Db	LysSerAspThrProCysAspAspPheThrArgCysProThrAsnAsnThrCysCysLys	378
1153	QY	CTCAGCTGCGGAGTGGGCTGCTGTCCAAATCCACAGAGCTGCTGCTCTCGGACCAC	1212
379	Db	LeuAsnSerGlyAspTrpGlyCysCysProIleProGluAlaValCysCysSerAspAsn	398
1213	QY	CAGCACTGCTCCCCCAGCATACACATGTGTGTAGCTGAGGGGAGTGTCCAGCAGGAAGC	1272
399	Db	GlnHisCysCysProGlnGlyPheThrCysLeuAlaGlnGlyTyrCysGlnLysGlyAsp	418
1273	QY	GAGATCGGTGTGACTGGAGAGATGCTTCCCGCGCGGGTTCCTTATCCACCCCAGA	1332
419	Db	ThrMetValAlaGlyLeuGluLysIleProAlaArgGlnThrThrProLeuGlnIleGly	438
1333	QY	GACATCGGCTGTGACCACACACAGCTGCCCGGTGGCGGAACTGTGCCCCGAGCCAG	1392
439	Db	AspIleGlyCysAspGlnHisThrSerCysProValGlyGlnThrCysCysProSerLeu	458
1393	QY	GGTGGAGCTGGGCTGTGTCAGTTGCCATGCTGTGTGCTCGGAGGATGCCAGAC	1452
459	Db	LysGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis	478
1453	QY	TGCTGCCGGCTGGCTACACTGTCGAACTGAAGCTCCATCCTCGAGAGGAAGTGTGC	1512
479	Db	CysCysProAlaGlyTyrThrCysAsnValLysAlaArgThrCysGluLysAspValAsp	498
1513	QY	TCTGCCACGCTGCCACCTTCTGTGCCCGGTAGCCCTCACGTGGGTGTGAAGACGTGGAG	1572

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Db      499  PheIleGlnProValLeuLeuThrLeuGlyProIlysValGly-----AsnValGlu 516
Qy      1573  TGTEGGGAAGGACACATTCTCCATGATAACACAGACCTGCTGCCGAGACACACCGACAGGC 1632
Db      517  CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysIysAspSerAlaGlyVal 536
Qy      1633  TGGGCCCTGCTCCCTACGCCGCCAGGGCGTCTGTTGCTGCTGATCGCGCCCACTGCTGCTCCT 1692
Db      537  TrpAlaCysCysProIyLeuIysGlyValCysCysArgaspGlyArgHisCysCysPro 556
Qy      1693  GCTGGCTTCGCTGCGCACGACGAGGGGTACCAAGTGTGTGGCGACGAGGAGCCCGCGCTGG 1752
Db      557  GlyGlyPheHisCysSerAlaArgGlyThrIysCysLeuArgIysIysIleProArgTrp 576
Qy      1753  GACGCCCTTTGAGGGACCCAGCCCTTGACAGCAGCTGCTG 1791
Db      577  AspMetPheLeuArgAspProValProArgProIleuLeu 589

RESULT 13
US-08-431-333-6
; Sequence 6, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Florman, Gregory D.
; TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,333
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO. 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 589 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-431-333-6

Alignment Scores:
Pred. No.: 1.55e-166 Length: 589
Score: 2693.00 Matches: 411
Percent Similarity: 83.98% Conservative: 57
Best Local Similarity: 74.37% Mismatches: 91
Query Match: 65.63% Indels: 4
DR. 2 Gaps: 3

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; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0071A-PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 728-4800
; TELEFAX: (206) 448-4775
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 589 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02321-6

Alignment Scores:
Pred. No.: 1.55e-166 Length: 589
Score: 2693.00 Matches: 441
Percent Similarity: 83.9% Conservative: 57
Best Local Similarity: 74.3% Mismatches: 91
Query Match: 65.6% Indels: 4
DB: 5 Gaps: 3

US-09-880-842-16 (1-2095) x PCT-US91-02321-6 (1-589)

QY 13 ATGTGACCCCTGCTGAGCTGGGTGGCTTAAACAGCAGGGCTGGTGGCTGGAAACGGGTGC 72
Db 1 MetTrrValLeuMetSerTrrPleuAlaPheAlaAlaGlyLeuValAlaGlyThrGlnCys 20
QY 73 CAGATGTCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132
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us-09-880-842-16.jun8.ra1

Wed Jun 9 09:59:50 2004

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GenCore version 5.1.6
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Searched: 1155919 seqs, 281338677 residues

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Minimum DB seq length: 0

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SUMMARIES

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3	3511	85.6	593	9	US-09-824-647-17	Sequence 17, Appl
4	3511	85.6	593	14	US-10-218-509-17	Sequence 17, Appl
5	3511	85.6	593	14	US-10-281-160-17	Sequence 17, Appl
6	3511	85.6	593	15	US-10-321-587-17	Sequence 17, Appl
7	3492	85.1	621	9	US-09-925-301-1416	Sequence 1416, Ap
8	3472	84.6	593	12	US-10-170-385-269	Sequence 269, App
9	3472	84.6	593	14	US-10-262-473-6	Sequence 6, Appli
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ALIGNMENTS

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; Sequence 17, Application US/09813156

; Patent No. US20020061859A1

; GENERAL INFORMATION:

; APPLICANT: Seriero, Ginette

; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

; FILE REFERENCE: Z9996.488/P001-A

; CURRENT APPLICATION NUMBER: US/09/813,156

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 08/991,862

; PRIOR FILING DATE: 1997-12-16

; PRIOR APPLICATION NUMBER: 08/863,862

; PRIOR FILING DATE: 1997-05-23

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 17

; LENGTH: 593

; TYPE: PRT

; ORGANISM: Human GP88 CDNA

; US-09-813-156-17

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; Patent No. US20020094966A1
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; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,807
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 593

! TYPE: PRT
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US-09-824-807-17

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QY 793 CTCCTCAAGAGAACGCTACACGACCTCTCTCACTAAGCTGCTGGCGCACAGTGGGC 852
DB 261 LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
QY 853 GATGTGAATGTGACATGAGTGGTGGCTGGCCAGATGGCTATACCTGCTCGCTACAG 912
DB 281 AspValLysCysAspMetGluValSerCysProAspGlyThrCysCysArgLeuGln 300

QY 913 TCGGGGCTGGGCTGCTGCCCTTTTACCCAGGCTGTGTGTGTGAGGACACATACAC 972
DB 301 SerGlyAlaIleTrpGlyCysCysProPheThrGlnAlaValCysCysGluAspHisIleHis 320
QY 973 TGCTGTCCCGCGGGGTTTACGTGTGACACGCAAGAGGGTACCTGTGAACAGGGGCCCCAC 1032
DB 321 CysCysProAlaGlyPheThrCysAspThrGlnLysGlyThrCysGluGlnGlyProHis 340
QY 1033 CAGGTGCCCTGATGGAGAGGCCCCAGCTCAGCTCAGCTGCGAGCCACACAGCCCTG 1092
DB 341 GlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeu 360
QY 1093 AAGAGAGATGTCCTCTGTCATATGTCAGCAGCTGTCCCTCTCCGATACCTGTGCCCCAA 1152
DB 361 LysArgAspValProCysAspAsnValSerSerCysProSerSerAspThrCysCysGln 380
QY 1153 CTCACGCTCGGGAGTGGGGCTGCTGTCACATCCACAGAGGCTGTCTGTCTCGGACCCAC 1212
DB 381 LeuThrSerGlyGluTrpGlyCysCysProIleProGluAlaValCysCysSerAspHis 400
QY 1213 CAGCACTGTGCCCCCAGCGATACAGTGTGTAGCTGAGGGGAGTGTCCAGCGAGGAGCC 1272
DB 401 GlnHisCysCysProGlnArgTrpThrCysValAlaGluGlyGlnCysGlnArgGlySer 420
QY 1273 GAGATCTGCTGCTGAGTGGAGAGATGCTGCCCGCGGGTTCCTTATCCACCCACAGA 1332
DB 421 GluIleValAlaGlyLeuGluLysMetProAlaArgArgGlySerLeuSerHisProArg 440
QY 1333 GACATCGGCTGTGACACACACACACAGCTGCCCGGTGGCGGAACTGTGTCGCCGAGCCAG 1392
DB 441 AspIleGlyCysAspGlnHisThrSerCysProValGlyThrCysCysProSerGln 460
QY 1393 GGTGGAGCTGGGCTGCTGCCAGTGTGCCCATGCTGTGTGTGTCGAGGATCGCCAGCAC 1452
DB 461 GlyGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis 480
QY 1453 TGTGCTGCCGCTGGCTACACCTGCAACGTGAAGGCTCGATCTCGGAGAGAGAGTGTCTC 1512
DB 481 CysCysProAlaGlyTrpThrCysAsnValLysAlaArgSerCysGluLysGluValVal 500
QY 1513 TCTGCCACGCTGCCACCTTCTCGGCCCTAGCCCTCAGCTGGGTGTGAAGACCTGGAG 1572
DB 501 SerAlaGlnProAlaThrPheLeuAlaArgSerProHisValGlyValLysAspValGlu 520
QY 1573 TGTGGGAAGAGCACTTCTGCCATGATACACAGACTGCTGCCGAGACACCGACAGGCG 1632
DB 521 CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysArgAspAsnArgGlnGly 540
QY 1633 TGGGCTGCTGCTCCCTACGCCAGGCGCTGTGTGTGTGATCGCGCCCTGCTGTCTCT 1692
DB 541 TrpAlaCysCysProTrpAlaGlnGlyValCysCysAlaAspArgHisCysCysPro 560
QY 1693 GCTGGCTTCGCTGGCAGCAGGAGGTACCAAGTGTTTTGGCAGGAGGCCCCCGCTGG 1752
DB 561 AlaGlyPheArgCysAlaArgGlyThrLysCysLeuArgArgGluAlaProArgTrp 580
QY 1753 GACGCCCTTTCAGGAGCCCGCTTGCAGCAGCTGCTG 1791
DB 581 AspAlaProLeuArgAspProAlaLeuArgGlnLeuLeu 593

RESULT 3

US-09-824-647-17
; Sequence 17, Application US/09824647
; Publication No. US20020183270A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,647
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17


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QY 1333 GACATCGGCTGTGACACACACACAGCTGCCCGGTGGGGGGAACCTGTGCTGCCCGAGCCAG 1392
Db 441 AsplleGlyCysAspGlnHisThrSerCysProValGlyGlnThrCysCysProSerLeu 460
QY 1393 GTGGGAGCTGGGCTGCTGCCAGCTGCCCATGTCTGTCTGCTGCAGAGATGCCAGCAC 1452
Db 461 GlyGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis 480
QY 1453 TGCTGCCCGCTGGCTACACCTGCAACGTGAAGGCTCGATCTGCGAGAGAAAGTGTCTC 1512
Db 481 CysCysProAlaGlyTyrThrCysAsnValLysAlaArgSerCysGluLysGluValVal 500
QY 1513 TGTGCCACCTGCCACCTTCTGCGCCGTAGCCCTCAGCTGGGTGTGAGAGACCTGGAG 1572
Db 501 SerAlaGlnProAlaThrPheLeuAlaArgSerProHisValGlyValLysAspValGlu 520
QY 1573 TGTGGGGAAGGACACTTCTGCCATGATACACAGACTGCTGCGCAGAGACACCGACAGGCG 1632
Db 521 CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysArgAspAsnArgGlnGly 540
QY 1633 TGGGCTGTGCTGCTCCCTACGCCAGGCGCTCTGTTGTGTGTGATCGCGGCCACTGTGCTCT 1692
Db 541 TrpAlaCysCysProTyrArgGlnGlyValCysCysAlaAspArgHisCysCysPro 560
QY 1693 GCTGGCTTCGCTGCGCACGACGAGGCTACCAAGTGTTCGCGAGAGGCGCCCGCGCTGG 1752
Db 561 AlaGlyPheArgCysAlaAlaArgGlyThrLysCysLeuArgArgGluAlaProArgTrp 580
QY 1753 GAGCGCCCTTTGAGGACCCAGCTTGTGAGACAGCTGCTG 1791
Db 581 AspAlaProLeuArgAspProAlaLeuArgGlnLeuLeu 593

RESULT 9
US-10-262-473-6
; Sequence 6, Application US/10262473
; Publication No. US20030199442A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John.
; APPLICANT: Burgess, Catherine.
; APPLICANT: Gorman, Linda.
; APPLICANT: Guo, Xiaojia.
; APPLICANT: Lepley, Denise.
; APPLICANT: Patturajan, Meera.
; APPLICANT: Rastelli, Luca.
; APPLICANT: Reiger, Daniel.
; APPLICANT: Spytek, Kimberly.
; APPLICANT: Zhong, Mei.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462B
; CURRENT APPLICATION NUMBER: US/10/262,473
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 6
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-473-6

Alignment Scores: 5.96e-195 Length: 593
Pred. No.: 3472.00 Matches: 587
Score:
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Percent Similarity: 98.99% Conservative: 0
Best Local Similarity: 98.99% Mismatches: 6
Query Match: 84.62% Indels: 0
DB: 14 Caps: 0

US-09-880-842-16 (1-2095) x US-10-262-473-6 (1-593)
QY 13 ATGTGACCCCTGTGTGAGCTGGGTGGGCTTAACAGCAGGAGCTGTGTGCTGGAAGCGGTGC 72
Db 1 MetTrpThrLeuValSerTrpValAlaLeuThrAlaGlyLeuValAlaGlyThrArgCys 20
QY 73 CCAGATGCTCAGTCTTCCGCTGTGGCTGTGCTGCGAGCCCCCGAGGAGCCAGCTACAGC 132
Db 21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer 40
QY 133 TGTGCGGCTCCCTTCTGTGACAAATGGCCCAACACTGAGCAGGATCTGGTGGTGGCCCC 192
Db 41 CysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHisLeuGlyGlyPro 60
QY 193 TGCAGGTTGATGCCACACTGCTGCGCGGCACTCTCTGCTATCTTTACCGTCTCAGGAGCT 252
Db 61 CysGlnValAspAlaHisCysSerAlaGlyHisSerCysAlaPheThrValSerGlyThr 80
QY 253 TCCAGTTGCTGCCCTTCCAGAGGCGGTGGCAGTGGGGGAGTGGCCATCATCTGCTGCCCA 312
Db 81 SerSerCysCysProPheProGluAlaValAlaCysGlyAspGlyHisCysCysPro 100
QY 313 CGGGCTTCCACTGCAGTGCAGACGCGGATCTGTTCCAAAGATCAGGTAAACAATCC 372
Db 101 ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnAsnSer 120
QY 373 GTGGGTGCCATCCAGTGCCTGTAGTACGTTCGAATGCCCGGACTTCTCCAGTGTCTGT 432
Db 121 ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys 140
QY 433 GTTATGTCATGCTCTGCGGGTGTGCTGCCATGCCCGGCTTCTCTGCTGTGAGAC 492
Db 141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp 160
QY 493 AGGGTGCACTGTGTCGCGACGCTCTTCTGCGACCTGTTCCACACCCGCTCATCACCA 552
Db 161 ArgValHisCysCysProHisGlyAlaPheCysAspLeuValHisThrArgCysIleThr 180
QY 553 CCCAGGGCACCCACCCCTGGGCAAGAGCTGCTGCCAGAGGACTACAGGCGAGTG 612
Db 181 ProThrGlyThrHisProLeuAlaLysLeuProAlaGlnArgThrAsnArgAlaVal 200
QY 613 GCCTTGTCCAGCTCGGTGTCGCGACGCGTCCCGGTCCCGTCTGATGGTCTTCTACC 672
Db 201 AlaLeuSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 220
QY 673 TGTGTGAGTGGCCCATGAGTGTGCTGCTGCCAATGCCCAAGCCAGCCAGCTGTGCTGC 732
Db 221 CysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsnAlaThrCysCys 240
QY 733 TCCGATCACCTGCACTGCTGCCCGCCCAAGACACTGTGTGTCACCTGATCCAGAGTAAGTG 792
Db 241 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys 260
QY 793 CTCTCCAGGAGAACGCTTACACGACCTCTCTACTAAGTGTGCTGGCGCACACAGTGGGC 852
Db 261 LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
QY 853 GATGTGAATGTGATGGAGGTGAGTGGCCAGATGCTATACCTGCTGCTGCTGCTACAG 912
Db 281 AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln 300
QY 913 TCGGGGGCTGCGGCTGCTGCCCTTTTACCAGGCTGTGTGCTGTGAGGACCAATACAC 972
Db 301 SerGlyAlaTrpGlyCysCysProPheThrGlnAlaValCysCysGluAspHisIleHis 320
QY 973 TGTCTTCCCGGGGTTCAGTGTGACACGAGGAGGTACTCTGTGACGGGGGCCCCAC 1032
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260	LeuSerLys---AsnTyrThrThraspLeuLeuThrLysLeuProGlyTyrProValLys	278
853	GATGTGAAATGTGACATGGAGGTGAGCTGCCAGATGGCTATACCTGCTGCCGTCTACAG	912
279	GlValLysCysAspMetGluValSerCysProGluGlyTyrThrCysCysArgLeuAsn	298
913	TCGGGGCCCTGGGGCTGCTGCTCCCTTTACCCAGCTGTGTGCTGTGAGGACCAATACAC	972
299	ThrGlyAlaTrpGlyCysCysProPheAlaLysAlaValCysCysAspAspHisIleHis	318
973	TGCTGTCCCGGGGTTTACGTGTGACACGCAGACAGGAGTACCTGTGTAAACAGGGGCCCCAC	1032
319	CysCysProAlaGlyPheGlnCysHisThrGluLysGlyThrCysGluMetGlyIleLeu	338
1033	CAGTGCCTCGATGGAGAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAAGCCTTG	1092
339	GlnValGlyTrpMetLysLysValIleAlaProLeuArgLeuProAspProGlnIleLeu	358
1093	AAGAGAGATGTCCTCTGTGTAATGTGACAGCTGTCCCTCCTCCGATACCTGCTGCCAA	1152
359	LysSerAspThrProCysAspAspPheThrArgCysProThrAsnAsnThrCysCysLys	378
1153	CTCACGTCTGGGAGTGGGGTGTCTGTCCTCAATCCACAGAGCTGTCCTGCTCGGACCAC	1212
379	LeuAsnSerGlyAspTrpGlyCysCysProIleProIleAlaValCysCysSerAspAsn	398
1213	CAGCACTGCTCCCCACGCATACACGTGTGTAGCTGAGGGCAGTGTACGAGGAGAC	1272
399	GlnHisCysCysProGlnGlyPheThrCysLeuAlaGlnGlyTyrCysGlnLysGlyAsp	418
1273	GAGATCGTGGCTGACCTGGAGAGATGCTGCCCCCGCGCGGTTCCTTATCCCACCCAGA	1332
419	ThrMetValAlaGlyLeuGluLysIleProAlaArgGlnThrThrProLeuGlnIleGly	438
1333	GACATCCGCTGTGACACGACACACAGCTGCCCGGTGGCGGAACTGCTGCCCGAGCCAG	1392
439	AspIleGlyCysAspGlnHisThrSerCysProValGlyGlnThrCysCysProSerLeu	458
1393	GGTGGAGCTGGGCTGCTGCCAGTGTGCCATGCTGTGCTGCTGCGAGAGTCCGACAC	1452
459	LysGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis	478
1453	TGCTGCCGCTGCTACCTGCAACGTGAGAGCTCGATCCTCCGAGAGAGAGTGGTC	1512
479	CysCysProAlaGlyTyrThrCysAsnValLysAlaArgThrCysGluLysAspValAsp	498
1513	TCGCCACAGCTGCCACTTCTCGCCCGTACGCCCTCAGCTGGGTGTGAAGGACCTGGAG	1572
499	PheIleGlnProProValLeuLeuThrLeuGlyProLysValGly-----AsnValGlu	516
1573	TGTGGGAAGACACTTCTGCCATGATAACAGACCTGCTGCCGAGACAACCCGACAGGGC	1632
517	CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysLysAspSerAlaGlyVal	536
1633	TGGGACCTGTCTCCCTACGCCAGGGCGTCTGTGTGCTGATCCGCGCCATGCTGTCCCT	1692
537	TrpAlaCysCysProTyrLeuLysGlyValCysCysArgAspGlyLysGlnHisCysCysPro	556
1693	GCTGGCTTCCGCTCGCACGAGGGGTACCAAGTGTGTGCGAGGAGGCCCGCCGCTGG	1752
557	GlyGlyPheHisCysSerAlaArgGlyThrLysCysLeuArgLysLysIleProArgTrp	576
1753	CACGCCCTTTGAGGAGCCCGAGCCTTGAGACAGCTGCTG	1791
577	AspMetPheLeuLysCysProValProArgProLeuLeu	589

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; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,647
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-09-824-647-2

Alignment Scores:
Pred. No.: 1,01e-148 Length: 589
Score: 2681.00 Matches: 439
Percent Similarity: 83.8% Conservative: 58
Best Local Similarity: 74.03% Mismatches: 92
Query Match: 65.34% Indels: 4
DB: 9 Gaps: 3

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US-09-880-842-16 (1-2095) x US-09-824-647-2 (1-589)

Qy	13	ATGTGACCTCGTCAGCTGGGTGGCTTAACACAGCGGTGGTGGCTGAACCGGTGC	72
Db	1	MetTpvAluWetSerTipLeuAlaPheAlaAlaGlyLeuValAlaGlyThrGlnCys	20
Qy	73	CCAGATGTCAGTTCTGCGCTGTGGCTGTGCTGACGCCCGAGAGACCACTACGC	132
Db	21	ProAspGlyGlnPheCysProValAlaCysCysLeuAspGlnGlyAlaAsnTyrSer	40
Qy	133	TGTCGCGTCCCTTCTCGCAAAATGGCCCAACACTGACAGGCATCTGGGTGGCCCC	192
Db	41	CysCysAenProLeuLeuAspThrTriProArgIleThrSerHisLeuAspGlySer	60
Qy	193	TGCCAGTTGATGCCCATGCTCTGCGCGGCACCTCTTCATCTTTACGCTCAGGACT	252
Db	61	CysGlnThrHisGlyHisCysProAlaGlyTyrSerCysLeuLeuThrValSerGlyThr	80
Qy	253	TCCAGTTGTGCGCCCTTCCAGAGCGCCGTGCATCGCGGGATGGCCATCACTCTGCCCA	312
Db	81	SerSerCysCysProPheSerIysGlyValSerCysGlyAspGlyTyrHisCysCysPro	100
Qy	313	CGGGGCTTCATGCAGTGCACAGCGGGATTCCTGCTTCCMAGATCAGGTAAACAATCC	372
Db	101	GlnGlyPheHisCysSerAlaAspGlySerCysPheGlnMetSer--AspAenPro	119
Qy	373	GTGGGTGCCATCCAGTGGCCCTGATAGTCAGATTCCAAATGCCGCACTTCTCCAGTGTGT	432
Db	120	LeuGlyAlaValGlnCysProGlySerGlnPheGlnCysProAspSerAlaThrCysCys	139
Qy	433	GTATGGTCGATGGCTCTCGGGGTGCTGCCCATGGCTCCCGAGGCTCTCTGCTGAAGAC	492
Db	140	IleMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp	159
Qy	493	AGGGTCACTGTCTCCGACAGCGTGCCTTCGCACTGTGTTACACCCGCTGCATCAC	552
Db	160	ArgValHisCysCysProHisGlyAlaSerCysAspLeuValHisThrArgCysValSer	179
Qy	553	CCACCGGGCACCCCTCGCAAGAGCTCCCTGCCGAGAGCACTAACAGGGCAGTG	612
Db	180	ProThrGlyThrHisThrLeuLeuIlysPheProAlaGlnIysThrAsnSerAlaVal	199
Qy	613	GCTCTGTCCAGTTCGTCATGTCCGACACCAAGTTCGCGGTGCCCTGTGTTCTTACC	672
Db	200	SerLeuProPheSerValValCysProAspAlaIysThrGlnCysProAspAspSerThr	219
Qy	673	TGCTGTGAGTCCCGAGTGGGAAGTATGGCTGTGCGCCCAATGCCCAACGCCACCTGCTGC	732
Db	220	CysCysGluLeuProThrGlyIysTyrGlyCysCysProMetProAsnAlaIleCysCys	239


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QY 733 TCCGATCACTGCTGCTGCCCCCAAGACACTGTGTGACCTGATCCAGAGTAAGTGC 792
Db 240 SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuLeuGlnSerLysCys 259
QY 793 CTCTCAAGAGAACCTTACCGACCTCTCTCACTAAGAGTCCCTGCGCACACAGTGGCC 852
Db 260 LeuSerLys---AsnTyrThrThrAspLeuLeuThrLysLeuProGlyTyrProValLys 278
QY 853 GATGTGAATGTGACATGGAGTGTGAGTCCAGATGGCTATACCTGTGCGCTACAG 912
Db 279 GluValLysCysAspMetGluValSerCysProGluGlyTyrThrCysCysArgLeuAsn 298
QY 913 TCGGGGCTGCGGCTGCTGCTGCTTTTACCAGGCTGTGTGTGAGGACCAATACAC 972
Db 299 ThrGlyAlaTrpGlyCysCysProPheAlaLysAlaValCysCysAspHisIleHis 318
QY 973 TCGTGTCCCGGGGTTTACGTGTGACAGCAGAGAGGTACTGTGACAGGGGCCAC 1032
Db 319 CysCysProAlaGlyPheGlnCysHisThrGluLysGlyThrCysGluMetGlyLeu 338
QY 1033 CAGGTGCTGATGAGAGAGCCCGACGCTCACTCCAGCTGCCAGACCCCAAGCTTG 1092
Db 339 GlnValGlyTrpMetLysLysValIleAlaProLeuArgLeuProAspProGlnIleLeu 358
QY 1093 AGAGAGATGCTCCCTGCTGATATGTACAGCAGTGTCTCTCCGATACCTGCGCAA 1152
Db 359 LysSerAspThrProCysAspAspPheThrArgCysProThrAsnAsnThrCysCysLys 378
QY 1153 CTCAGTCTGCGGAGTGGGGCTGCTGCTCCAAATCCACAGAGGCTGTCTGTCTCGACAC 1212
Db 379 LeuAsnSerGlyAspTrpGlyCysCysProIleProGluAlaValCysCysSerAspAsn 398
QY 1213 CAGCACTGTGCTCCCGCAGGATACAGTGTGTAGTGTGAGGGCAGTGTACGGAGGAGC 1272
Db 399 GlnHisCysCysProGlnGlyPheThrCysLeuAlaGlnGlyTyrCysGlnLysGlyAsp 418
QY 1273 GAGATCGTGGCTGAGTGGAGAGATGCTGCTGCCCGCGGTTCTTATCCACCCACA 1332
Db 419 ThrMetValAlaGlyLeuGluLysIleProAlaArgGlnThrThrProLeuGlnIleGly 438
QY 1333 GACATGGTGTGACAGACACACAGTGTGCTGCGGGGGGAACTGTGCTGCGCGAGCAG 1392
Db 439 AspIleGlyCysAspGlnHisThrSerCysProValGlyGlnThrCysCysProSerLeu 458
QY 1393 GGTGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1452
Db 459 LysGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis 478
QY 1453 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1512
Db 479 CysCysProAlaGlyTyrThrCysAsnValLysAlaArgThrCysGluLysAspValAsp 498
QY 1513 TCTGCGCAGCTGCCACTTCTGCGCGCTAGCCCTCAGCTGGGTGTGAGGACGTGGAG 1572
Db 499 PheIleGlnProProValLeuLeuThrLeuGlyProLysValGly-----AsnValGlu 516
QY 1573 TGTGGGAAGGACACTTCTGCCATGATACAGACCTGTGCTGCCGAGACCAACCGACAGGC 1632
Db 517 CysGlyGluGlyHisPheCysHisAspAsnGlnThrCysCysLysAspSerAlaGlyVal 536
QY 1633 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1692
Db 537 TrpAlaCysCysProTyrLeuLysGlyValCysCysArgAspGlyArgHisCysCysPro 556
QY 1693 GCTGGCTTCCGCTGCCAGCAGGAGGTACCAAGTGTTCGCGAGGAGGCGCGGCTGG 1752
Db 557 GlyGlyPheHisCysSerAlaArgGlyThrLysCysLeuArgLysIleProArgTrp 576
QY 1753 GAGCCCTTTGAGGAGCCCGCTTGTGAGAGAGTGTGCTG 1791
Db 577 AspMetPheLeuArgAspProValProArgProLeuLeu 589
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RESULT 13

US-10-218-509-2
; Sequence 2, Application US/10218509
; Publication No. US20030092661A1
; GENERAL INFORMATION:

; APPLICANT: Serreto, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCES: 29996.488/2001-A
; CURRENT APPLICATION NUMBER: US/10/218,509
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 08/391,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

; LENGTH: 589
; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-10-218-509-2

Alignment Scores:

Pred. No.:	1,01e-148	Length:	589
Score:	2681.00	Matches:	439
Percent Similarity:	83.81%	Conservative:	58
Best Local Similarity:	74.03%	Mismatches:	92
Query Match:	65.34%	Indels:	4
DB:	14	Gaps:	3

US-09-880-842-16 (1-2095) x US-10-218-509-2 (1-589)

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QY 13 ATGTGACCTGTGTGAGTGGTGGCTTAACAGAGGCTGTGTGCTGGAAGCGGTGC 72
Db 1 MetTrpValLeuMetSerTrpLeuAlaPheAlaGlyLeuValAlaGlyThrGlnCys 20
QY 73 CCAGATGTCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132
Db 21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspGlnGlyAlaAsnTyrSer 40
QY 133 TGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
Db 41 CysCysAsnProLeuLeuAspThrTrpProArgIleThrSerHisLeuAspGlySer 60
QY 193 TGCCAGGTTCATGCCACTGCTGCTGCGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
Db 61 CysGlnThrHisGlyHisCysProAlaGlyTyrSerCysLeuLeuThrValSerGlyThr 80
QY 253 TCCAGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
Db 81 SerSerCysCysProPheSerLysGlyValSerCysGlyAspGlyTyrHisCysCysPro 100
QY 313 CGGGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
Db 101 GlnGlyPheHisCysSerAlaAspGlyLysSerCysPheGlnMetSer---AspAsnPro 119
QY 373 GTGGGTGCCATCCAGTGCCTGATGATGCTTCCAAATGCCCGGACTTCTCCAGTGTCTGT 432
Db 120 LeuGlyAlaValGlnCysProGlySerGlnPheGluCysProAspSerAlaThrCysCys 139
QY 433 GTTATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492
Db 140 IleMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp 159
QY 493 AGGTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
Db 160 ArgValHisCysCysProHisGlyAlaSerCysAspLeuValHisThrArgCysValSer 179
QY 553 CCGACGGGCGCCACCCCTGGCAAGAGTCCCTGCCAGAGGACTTAACAGGAGGAGTGC 612
Db 180 ProThrGlyThrHisThrLeuLeuLysLysPheProAlaGlnLysThrAsnSerAlaVal 199
QY 613 GCCTGTGCCAGCTCGGTCACTGTGCTGCGGACGACGCTGCCGCTGCCCTGATGCTTCTACC 672
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200	Db	200	SeqLeuProPheSerValValCysProAspAlaIysThrGlnCysProAspAspSerThr	219
673	QY	673	TGCTGTGAGCTGCCAGTGGGAAGTAGCTGCTGTGCCAATGCCCCAACGCCACTGCTGC	732
220	Db	220	CysCysGlnLeuProThrGlyLysTyrglyCysCysProMetProAsnAlaIleCysCys	239
733	QY	733	TCCGATCACCTGCAGCTGCTGCCCCCAAGACACACTGTGTGCTACCTGCATCCAGAGTAAGTGC	792
240	Db	240	SerAspHisLeuHisCysCysProGlnAspThrValCysAspLeuIleGlnSerLysCys	259
793	QY	793	CTCTCCAAGGAGAACGCTACCCAGGACCTCTCACTAAGCTGCTGGCCGACACAGTGGGC	852
260	Db	260	LeuSerLys--AanTyThrThrAspLeuLeuThrLysLeuProGlyTyProValLys	278
853	QY	853	GATGTGAATGTGACATGGAGGTGAGTGGCCAGATGGCTATACCTGCTGCGCTTACAG	912
279	Db	279	GlnValLysCysAspMetGluValSerCysProGlnGlyTyThrCysCysArgLeuAsn	298
913	QY	913	TCGGGGCCCTGGGGCTGCTGCCCTTTTACCAGGCTGTGTGCTGAGGACCAATACAC	972
299	Db	299	ThrGlyAlaTrpGlyCysCysProPheAlaIysAlaValCysCysAspAspHisIleHis	318
973	QY	973	TGCTGTCCCGGGGTTTACGTGTGACACGACGAGGGTACCTGTGTGAACAGGGGCCCCAC	1032
319	Db	319	CysCysProAlaGlyPheGlnCysHisThrGlnLysGlyThrCysGlnMetGlyIleLeu	338
1033	QY	1033	CAGTGCCTCGGATGGAGAGAGGCCCCAGCTCACCTCAGCTGCCAGACCCACACAGCCCTG	1092
339	Db	339	GlnValGlyTrpMetLysLysValIleAlaProLeuArgLeuProAspProGlnIleLeu	358
1093	QY	1093	AAGAGAGATGCCCTCTGTGATAATGTTCAGCAGCTGTCCCTCCCTCCGATACCTGCTGCA	1152
359	Db	359	LysSerAspThrProCysAspAspPheThrArgCysProThrAenAenThrCysCysLys	378
1153	QY	1153	CTCAGCTCTGGGAGTGGGGCTGTGTGCCAATCCAGAGCTGCTGCTGCTCGGACAC	1212
379	Db	379	LeuAsnSerGlyAspTrpGlyCysCysProIleProGlnAlaValCysCysSerAspAsn	398
1213	QY	1213	CAGCACCTGCTGCCCCACGACATACACGTGTGTAGCTGAGGGGACGTGTCCAGCAGGAGC	1272
399	Db	399	GlnHisCysCysProGlnGlyPheThrCysLeuAlaGlnGlyTyThrCysGlnLysGlyAsp	418
1273	QY	1273	GAGATCGTGGCTGGAGTGGAGAGATGCCTGCCCGCGGGTTCCTTATCCACCCCAGA	1332
419	Db	419	ThrMetValAlaGlyLeuGluLysIleProAlaArgGlnThrThrProLeuGlnIleGly	438
1333	QY	1333	GACATCGGCTGTGACACGACACACAGCTGCCCGGTGGCGGAACTGCTGCCGAGGCAG	1392
439	Db	439	AspIleGlyCysAspGlnHisThrSerCysProValGlyGlnThrCysCysProSerLeu	458
1393	QY	1393	GGTGGGAGCTGGGGCTGCTGCCATTGCCCATGCTGTGTGCTGCGAGGATGCCAGCAC	1452
459	Db	459	LysGlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHis	478
1453	QY	1453	TGCTGCCCGCTGCTACACTGACCTGCAACGTGAAGCTCGATCCTCCGAGAGAAGTGCCTC	1512
479	Db	479	CysCysProAlaGlyTyThrCysAsnValLysAlaArgThrCysGlnLysAspValAsp	498
1513	QY	1513	TCTCCCGAGCTGCCACTCTCTGGCCCGCTAGCCCTCACGTGGGTGTGAAGACGTGGAG	1572
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537	Db	537	TrpAlaCysCysProTyTrpLeuLysGlyValCysCysArgAspGlyArgHisCysCysPro	556
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557	Db	557	GlyGlyPheHisCysSerAlaArgGlyThrLysCysLeuArgLysLysIleProArgTrp	576

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; Sequence 2, Application US/10281160			
; Publication No. US20030108950A1			
; GENERAL INFORMATION:			
; APPLICANT: Seriero, Ginette			
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AN			
; FILE REFERENCE: Z9996.48B/P001-A			
; CURRENT APPLICATION NUMBER: US/10/281.160			
; CURRENT FILING DATE: 2002-10-28			
; PRIOR APPLICATION NUMBER: US/08/991,862			
; PRIOR FILING DATE: 1998-08-17			
; PRIOR APPLICATION NUMBER: 08/863,862			
; PRIOR FILING DATE: 1997-05-23			
; NUMBER OF SEQ ID NOS: 17			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 2			
; LENGTH: 589			
; TYPE: PRT			
; ORGANISM: Mouse epithelin/granulin			
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Alignment Scores:			
Pred. No.: 1.01e-148 Length: 589			
Score: 2681.00 Matches: 439			
Percent Similarity: 83.81% Conservative: 58			
Best Local Similarity: 74.03% Mismatches: 92			
Query Match: 65.34% Indels: 4			
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Db	41	CysCysAsnProLeuLeuAspThrTrpProArgIleThrSerHis	
Qy	193	TGCCAGGTGTAGCCCACTGCTCTGCCGGCCACTCTCTGCATCTT	
Db	61	CysGlnThrHisGlyHisCysProAlaGlyTySerCysLeuLeu	
Qy	253	TCCAGTTGTCCTCCCTCCAGAGCCCGTGGCATGCGGGATGGG	
Db	81	SerSerCysCysProPheSerLysGlyValSerCysGlyAspGly	
Qy	313	CGGGGCTTCCACTGTCAGTCAGCAGCGGGCGATCTCTTCCAAAG	
Db	101	GlnGlyPheHisCysSerAlaAspGlyIleSerCysPheGlnMet	
Qy	373	GTGGGTGCATCCAGTGCCTGTAGTAGTCAGTTGCAATGCCCGG	
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Db 140 IleMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp 159
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QY 553 CCACCGGGACCCACACCCCTGGCAAGAGCTCCCTGCCAGAGACTAACAGGGCAGTG 612
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Search completed: June 8, 2004, 17:05:43
Job time : 147 secs

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